

```

1  AAGTAAAAGAAAGAGCGAGAAATCATCGAAATGGATTTCATCTCATCTCTTATCGTTGGC
   -----+-----+-----+-----+-----+-----+-----+ 60
   TTCATTTTCTTTCTCGCTCTTTAGTAGCTTTACCTAAAGTAGAGTAGAGAATAGCAACCG

a  K * K K E R E I I E (M) D F I S S L I V G -
b  S K R K S E K S S K W I S S H L L S L A -
c  V K E R A R N H R N G F H L I S Y R W L -

   TGTGCTCAGGTGTTGTGTGAATCTATGAATATGGCGGAGAGAAGAGGACATAAGACTGAT
61 -----+-----+-----+-----+-----+-----+ 120
   ACACGAGTCCACAACACACTTAGATACTTATACCGCCTCTCTTCTCCTGTATTCTGACTA

a  C A Q V L C E S M N M A E R R G H K T D -
b  V L R C C V N L * I W R R E E D I R L I -
c  C S G V V * I Y E Y G G E K R T * D * S -

   CTTAGACAAGCCATCACTGATCTTGAAACAGCCATCGGTGACTTGAAGGCCATACGTGAT
121 -----+-----+-----+-----+-----+-----+ 180
   GAATCTGTTTCGGTAGTGACTAGAACTTTGTCGGTAGCCACTGAACTTCCGGTATGCACTA

a  L R Q A I T D L E T A I G D L K A I R D -
b  L D K P S L I L K Q P S V T * R P Y V M -
c  * T S H H * S * N S H R * L E G H T * * -

   GACCTGACTTTACGGATCCAACAAGACGGTCTAGAGGGACGAAGCTGCTCAAATCGTGCC
181 -----+-----+-----+-----+-----+-----+ 240
   CTGGACTGAAATGCCTAGGTTGTTCTGCCAGATCTCCCTGCTTCGACGAGTTTAGCACGG

a  D L T L R I Q Q D G L E G R S C S N R A -
b  T * L Y G S N K T V * R D E A A Q I V P -
c  P D F T D P T R R S R G T K L L K S C Q -

   AGAGAGTGGCTTAGTGCGGTGCAAGTAACGGAGACTAAAACAGCCCTACTTTTAGTGAGG
241 -----+-----+-----+-----+-----+-----+ 300
   TCTCTACCGAATCACGCCACGTTTCATTGCCTCTGATTTTGTCTGGGATGAAAATCACTCC

a  R E W L S A V Q V T E T K T A L L L V R -
b  E S G L V R C K * R R L K Q P Y F * * G -
c  R V A * C G A S N G D * N S P T F S E V -

   TTTAGGCGTCGGGAACAGAGGACGCGAATGAGGAGGAGATACCTCAGTTGTTTCGGTTGT
301 -----+-----+-----+-----+-----+-----+ 360
   AAATCCGCAGCCCTTGTCTCCTGCGCTTACTCCTCCTCTATGGAGTCAACAAAGCCAACA

a  F R R R E Q R T R M R R R Y L S C F G C -
b  L G V G N R G R E * G G D T S V V S V V -
c  * A S G T E D A N E E E I P Q L F R L C -

   GCCGACTACAACTGTGCAAGAAGGTTTCTGCCATATTGAAGAGCATTGGTGAGCTGAGA
361 -----+-----+-----+-----+-----+-----+ 420
   CGGCTGATGTTTGACACGTTCTTCCAAAGACGGTATAACTTCTCGTAACCACTCGACTCT

```

Fig. 2A

```

a  A D Y K L C K K V S A I L K S I G E L R -
b  P T T N C A R R F L P Y * R A L V S * E -
c  R L Q T V Q E G F C H I E E H W * A E R -

GAACGCTCTGAAGCTATCAAAACAGATGGCGGGTCAATTCAAGTAACTTGTAGAGAGATA
421 -----+-----+-----+-----+-----+ 480
CTTGCGAGACTTCGATAGTTTTGTCTACCGCCCAGTTAAGTTCATTGAACATCTCTCTAT

a  E R S E A I K T D G G S I Q V T C R E I -
b  N A L K L S K Q M A G Q F K * L V E R Y -
c  T L * S Y Q N R W R V N S S N L * R D T -

CCCATCAAGTCCGTTGTCGGAAATACCACGATGATGGAACAGGTTTTGGAATTTCTCAGT
481 -----+-----+-----+-----+-----+ 540
GGGTAGTTCAGGCAACAGCCTTTATGGTGCTACTACCTTGTCCAAAACCTTAAAGAGTCA

a  P I K S V V G N T T M M E Q V L E F L S -
b  P S S P L S E I P R * W N R F W N F S V -
c  H Q V R C R K Y H D D G T G F G I S Q * -

GAAGAAGAAGAAAGAGGAATCATTGGTGTTTATGGACCTGGTGGGGTTGGGAAGACAACG
541 -----+-----+-----+-----+-----+ 600
CTTCTTCTTCTTTCTCCTTAGTAACCACAAATACCTGGACCACCCCAACCCTTCTGTTGC

a  E E E E R G I I G V Y G P G G V G K T T -
b  K K K K E E S L V F M D L V G L G R Q R -
c  R R R K R N H W C L W T W W G W E D N V -

TTAATGCAGAGCATTAAACAACGAGCTGATCACAAAAGGACATCAGTATGATGTACTGATT
601 -----+-----+-----+-----+-----+ 660
AATTACGTCTCGTAATTGTTGCTCGACTAGTGTTTTCTGTAGTCATACTACATGACTAA

a  L M Q S I N N E L I T K G H Q Y D V L I -
b  * C R A L T T S * S Q K D I S M M Y * F -
c  N A E H * Q R A D H K R T S V * C T D L -

TGGGTTCAAATGTCCAGAGAATTCGGCGAGTGTAACAATTCAGCAAGCCGTTGGAGCACGG
661 -----+-----+-----+-----+-----+ 720
ACCCAAGTTTACAGGTCTCTTAAGCCGCTCACATGTTAAGTCGTTGGCAACCTCGTGCC

a  W V Q M S R E F G E C T I Q Q A V G A R -
b  G F K C P E N S A S V Q F S K P L E H G -
c  G S N V Q R I R R V Y N S A S R W S T V -

TTGGGTTTATCTTGGGACGAGAAGGAGACCGGCGAAAACAGAGCTTTGAAGATATACAGA
721 -----+-----+-----+-----+-----+ 780
AACCCAAATAGAACCCTGCTCTTCTCTGGCCGCTTTTGTCTCGAAACTTCTATATGTCT

a  L G L S W D E K E T G E N R A L K I Y R -
b  W V Y L G T R R R P A K T E L * R Y T E -
c  G F I L G R E G D R R K Q S F E D I Q S -

GCTTTGAGACAGAAACGTTTCTTGTGTTGCTAGATGATGTCTGGGAAGAGATAGACTTG
781 -----+-----+-----+-----+-----+ 840
CGAAACTCTGTCTTTGCAAAGAACAACAACGATCTACTACAGACCCTTCTCTATCTGAAC

```

Fig. 2B

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a  A L R Q   R F L L L L D D V W E E I D L -
b  L * D R   I V S C C C * M M S G K R * T W -
c  F E T     T F L V V A R * C L G R D R L G -

GAGAAACTGGAGTTCCTCGACCTGACAGGGAAACAAATGCAAGGTGATGTTACGACA
841 -----+-----+-----+-----+-----+-----+ 900
CTCTTTTGACCTCAAGGAGCTGGACTGTCCCTTTTGTTCACGTTCCACTACAAGTGCTGT

a  E K T G V P R P D R E N K C K V M F T T -
b  R K L E F L D L T G K T N A R * C S R H -
c  E N W S S S T * Q G K Q M Q G D V H D T -

CGGTCTATAGCATTATGCAACAATATGGGTGCGGAATACAAGTTGAGAGTGGAGTTTCTG
901 -----+-----+-----+-----+-----+-----+ 960
GCCAGATATCGTAATACGTTGTTATACCCACGCCTTATGTTCAACTCTCACCTCAAAGAC

a  R S I A L C N N M G A E Y K L R V E F L -
b  G L * H Y A T I W V R N T S * E W S F W -
c  V Y S I M Q Q Y G C G I Q V E S G V S G -

GAGAAGAAACACGCGTGGGAGCTGTTCTGTAGTAAGGTATGGAGAAAAGATCTTTTAGAG
961 -----+-----+-----+-----+-----+-----+ 1020
CTCTTCTTTGTGCGCACCTCGACAAGACATCATTCCATACCTCTTTTCTAGAAAATCTC

a  E K K H A W E L F C S K V W R K D L L E -
b  R R N T R G S C S V V R Y G E K I F * S -
c  E E T R V G A V L * * G M E K R S F R V -

TCATCATCAATTGCGCGGCTCGCGGAGATTATAGTGAGTAAATGTGGAGGATTGCCACTA
1021 -----+-----+-----+-----+-----+-----+ 1080
AGTAGTAGTTAAGCGGCGGAGCGCCTCTAATATCACTCATTTACACCTCCTAACGGTGAT

a  S S S I R R L A E I I V S K C G G L P L -
b  H H Q F A G S R R L * * V N V E D C H * -
c  I I N S P A R G D Y S E * M W R I A T S -

GCGTTGATCACTTTAGGAGGAGCCATGGCTCATAGAGAGACAGAAGAAGAGTGGATCCAT
1081 -----+-----+-----+-----+-----+-----+ 1140
CGCAACTAGTGAAATCCTCCTCGGTACCGAGTATCTCTCTGTCTTCTTCTCACCTAGGTA

a  A L I T L G G A M A H R E T E E E W I H -
b  R * S L * E E P W L I E R Q K K S G S M -
c  V D H F R R S H G S * R D R R R V D P C -

GCTAGTGAAGTTCTGACTAGATTTCCAGCAGAGATGAAGGGTATGAACTATGTATTTGCC
1141 -----+-----+-----+-----+-----+-----+ 1200
CGATCACTTCAAGACTGATCTAAAGGTCGTCTCTACTTCCCATACTTGATACATAAACGG

a  A S E V L T R F P A E M K G M N Y V F A -
b  L V K F * L D F Q Q R * R V * T M Y L P -
c  * * S S D * I S S R D E G Y E L C I C P -

CTTTTGAAATTCAGCTACGACAACCTCGAGAGTGATCTGCTTCGGTCTTGTTCCTTGAC
1201 -----+-----+-----+-----+-----+-----+ 1260
GAAAACTTTAAGTCGATGCTGTTGGAGCTCTCACTAGACGAAGCCAGAACAAGAACATG

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Fig. 2C

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a   L L K F S Y D N L E S D L L R S C F L Y -
b   F * N S A T T T S R V I C F G L V S C T -
c   F E I Q L R Q P R E * S A S V L F L V L -

      TGCGCTTTATTCCCAGAAGAACATTCTATAGAGATCGAGCAGCTTGTTGAGTACTGGGTC
1261 -----+-----+-----+-----+-----+-----+ 1320
      ACGCGAAATAAGGGTCTTCTTGTAAGATATCTCTAGCTCGTCAACAACTCATGACCCAG

a   C A L F P E E H S I E I E Q L V E Y W V -
b   A L Y S Q K N I L * R S S S L L S T G S -
c   R F I P R R T F Y R D R A A C * V L G R -

      GGCGAAGGGTTTCTCACCAGCTCCCATGGCGTTAACACCATTTACAAGGGATATTTTCTC
1321 -----+-----+-----+-----+-----+-----+ 1380
      CCGCTTCCCAAAGAGTGGTCGAGGGTACCGCAATTGTGGTAAATGTTCCCTATAAAAGAG

a   G E G F L T S S H G V N T I Y K G Y F L -
b   A K G F S P A P M A L T P F T R D I F S -
c   R R V S H Q L P W R * H H L Q G I F S H -

      ATTGGGGATCTGAAAGCGGCATGTTTGTGGAACCGGAGATGAGAAAACACAGGTGAAG
1381 -----+-----+-----+-----+-----+-----+ 1440
      TAACCCCTAGACTTTTCGCCGTACAAACAACCTTTGGCCTCTACTCTTTTGTGTCCACTTC

a   I G D L K A A C L L E T G D E K T Q V K -
b   L G I * K R H V C W K P E M R K H R * R -
c   W G S E S G M F V G N R R * E N T G E D -

      ATGCATAATGTGGTCAGAAGCTTTGCATTGTGGATGGCATCTGAACAGGGGACTTATAAG
1441 -----+-----+-----+-----+-----+-----+ 1500
      TACGTATTACACCAGTCTTCGAAACGTAACACCTACCGTAGACTTGTCCCCTGAATATTC

a   M H N V V R S F A L W M A S E Q G T Y K -
b   C I M W S E A L H C G W H L N R G L I R -
c   A * C G Q K L C I V D G I * T G D L * G -

      GAGCTGATCCTAGTTGAGCCTAGCATGGGACATACTGAAGCTCCTAAAGCAGAAAACCTGG
1501 -----+-----+-----+-----+-----+-----+ 1560
      CTCGACTAGGATCAACTCGGATCGTACCCTGTATGACTTCGAGGATTTTCGTCTTTTGACC

a   E L I L V E P S M G H T E A P K A E N W -
b   S * S * L S L A W D I L K L L K Q K T G -
c   A D P S * A * H G T Y * S S * S R K L A -

      CGACAAGCGTTGGTGATCTCATTGTTAGATAACAGAATCCAGACCTTGCCTGAAAAACTC
1561 -----+-----+-----+-----+-----+-----+ 1620
      GCTGTTGCAACCACTAGAGTAACAATCTATTGTCTTAGGTCTGGAACGGACTTTTGTAG

a   R Q A L V I S L L D N R I Q T L P E K L -
b   D K R W * S H C * I T E S R P C L K N S -
c   T S V G D L I V R * Q N P D L A * K T H -

```

Fig. 2D

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ATATGCCCCGAAACTGACAACACTGATGCTCCAACAGAACAGCTCTTTGAAGAAGATTCCA
1621 -----+-----+-----+-----+-----+-----+ 1680
TATACGGGCTTTGACTGTTGTGACTACGAGGTTGTCTTGTGCGAGAACTTCTTCTAAGGT

a   I C P K L T T L M L Q Q N S S L K K I P -
b   Y A R N * Q H * C S N R T A L * R R F Q -
c   M P E T D N T D A P T E Q L F E E D S N -

ACAGGGTTTTTTCATGCATATGCCTGTTCTCAGAGTCTTGGACTTGTCGTTTACAAGTATC
1681 -----+-----+-----+-----+-----+-----+ 1740
TGTCCCAAAAAGTACGTATACGGACAAGAGTCTCAGAACCTGAACAGCAAGTGTTTCATAG

a   T G F F M H M P V L R V L D L S F T S I -
b   Q G F S C I C L F S E S W T C R S Q V S -
c   R V F H A Y A C S Q S L G L V V H K Y H -

ACTGAGATTCCGTTGTCTATCAAGTATTTGGTGGAGTTGTATCATCTGTCTATGTCAGGA
1741 -----+-----+-----+-----+-----+-----+ 1800
TGACTCTAAGGCAACAGATAGTTCATAAACCACCTCAACATAGTAGACAGATACAGTCCT

a   T E I P L S I K Y L V E L Y H L S M S G -
b   L R F R C L S S I W W S C I I C L C Q E -
c   * D S V V Y Q V F G G V V S S V Y V R N -

ACAAAGATAAGTGTATTGCCACAGGAGCTTGGGAATCTTAGAAAACCTGAAGCATCTGGAC
1801 -----+-----+-----+-----+-----+-----+ 1860
TGTTTTCTATTACATAACGGTGTCTCTCGAACCCCTTAGAATCTTTTGACTTCGTAGACCTG

a   T K I S V L P Q E L G N L R K L K H L D -
b   Q R * V Y C H R S L G I L E N * S I W T -
c   K D K C I A T G A W E S * K T E A S G P -

CTACAAAGAACTCAGTTTCTTCAGACGATCCCACGAGATGCCATATGTTGGCTGAGCAAG
1861 -----+-----+-----+-----+-----+-----+ 1920
GATGTTTCTTGAGTCAAAGAAGTCTGCTAGGGTGCTCTACGGTATACAACCGACTCGTTC

a   L Q R T Q F L Q T I P R D A I C W L S K -
b   Y K E L S F F R R S H E M P Y V G * A S -
c   T K N S V S S D D P T R C H M L A E Q A -

CTCGAGGTTCTGAACTTGTA CTACTACAGTTACGCCGGTTGGGAACTGCAGAGCTTTGGAGAA
1921 -----+-----+-----+-----+-----+-----+ 1980
GAGCTCCAAGACTTGAACATGATGTCAATGCGGCCAACCCCTTGACGTCTCGAAACCTCTT

a   L E V L N L Y Y S Y A G W E L Q S F G E -
b   S R F * T C T T V T P V G N C R A L E K -
c   R G S E L V L Q L R R L G T A E L W R R -

GATGAAGCAGAAGAACTCGGATTCGCTGACTTGGAATACTTGGAACCTAACCACACTC
1981 -----+-----+-----+-----+-----+-----+ 2040
CTACTTCGTCTTCTTGAGCCTAAGCGACTGAACCTTATGAACCTTTTGGATTGGTGTGAG

```

Fig. 2E

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a   D E A E E L G F A D L E Y L E N L T T L -
b   M K Q K N S D S L T W N T W K T * P H S -
c   * S R R T R I R * L G I L G K P N H T R -

GGTATCACTGTTCTCTCATTGGAGACCCTAAAACTCTCTTCGAGTTCGGTGCTTTGCAT
2041 -----+-----+-----+-----+-----+-----+ 2100
CCATAGTGACAAGAGAGTAACCTCTGGGATTTTTGAGAGAAGCTCAAGCCACGAAACGTA

a   G I T V L S L E T L K T L F E F G A L H -
b   V S L F S H W R P * K L S S S S V L C I -
c   Y H C S L I G D P K N S L R V R C F A * -

AAACATATACAGCATCTCCACGTTGAAGAGTGCAATGAACTCCTCTACTTCAATCTCCCA
2101 -----+-----+-----+-----+-----+-----+ 2160
TTTGTATATGTCGTAGAGGTGCAACTTCTCACGTTACTTGAGGAGATGAAGTTAGAGGGT

a   K H I Q H L H V E E C N E L L Y F N L P -
b   N I Y S I S T L K S A M N S S T S I S H -
c   T Y T A S P R * R V Q * T P L L Q S P I -

TCACTCACTAACCATGGCAGGAACCTGAGAAGACTTAGCATTAAAAGTTGCCATGACTTG
2161 -----+-----+-----+-----+-----+-----+ 2220
AGTGAGTGATTGGTACCGTCCTTGGACTCTTCTGAATCGTAATTTTCAACGGTACTGAAC

a   S L T N H G R N L R R L S I K S C H D L -
b   H S L T M A G T * E D L A L K V A M T W -
c   T H * P W Q E P E K T * H * K L P * L G -

GAGTACCTGGTCACACCCGCAGATTTTGAAAATGATTGGCTTCCGAGTCTAGAGGTTCTG
2221 -----+-----+-----+-----+-----+-----+ 2280
CTCATGGACCAGTGTGGGCGTCTAAACTTTTACTAACCGAAGGCTCAGATCTCCAAGAC

a   E Y L V T P A D F E N D W L P S L E V L -
b   S T W S H P Q I L K M I G F R V * R F * -
c   V P G H T R R F * K * L A S E S R G S D -

ACGTTACACAGCCTTCACAACCTTAACCAGAGTGTGGGGAAATTCTGTAAGCCAAGATTGT
2281 -----+-----+-----+-----+-----+-----+ 2340
TGCAATGTGTGCGAAGTGTGAATTGGTCTCACACCCCTTTAAGACATTCGGTTCTAACA

a   T L H S L H N L T R V W G N S V S Q D C -
b   R Y T A F T T * P E C G E I L * A K I V -
c   V T Q P S Q L N Q S V G K F C K P R L S -

CTGCGGAATATCCGTTGCATAAACATTTCACTGCAACAAGCTGAAGAATGTCTCATGG
2341 -----+-----+-----+-----+-----+-----+ 2400
GACGCCTTATAGGCAACGTATTTGTAAAGTGTGACGTTGTTTCGACTTCTTACAGAGTACC

a   L R N I R C I N I S H C N K L K N V S W -
b   C G I S V A * T F H T A T S * R M S H G -
c   A E Y P L H K H F T L Q Q A E E C L M G -

GTTCAGAAACTCCCAAAGCTAGAGGTGATTGAACTGTTGACTGCAGAGAGATAGAGGAA
2401 -----+-----+-----+-----+-----+-----+ 2460
CAAGTCTTTGAGGGTTTCGATCTCCACTAACTTGACAAGCTGACGTCTCTCTATCTCCTT

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Fig. 2F

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a  V Q K L P K L E V I E L F D C R E I E E -
b  F R N S Q S * R * L N C S T A E R * R N -
c  S E T P K A R G D * T V R L Q R D R G I -

TTGATAAGCGAACACGAGAGTCCATCCGTCGAAGATCCAACATTGTTCCCAAGCCTGAAG
2461 -----+-----+-----+-----+-----+-----+-----+ 2520
AACTATTCGCTTGTGCTCTCAGGTAGGCAGCTTCTAGGTTGTAACAAGGGTTCGGACTTC

a  L I S E H E S P S V E D P T L F P S L K -
b  * * A N T R V H P S K I Q H C S Q A * R -
c  D K R T R E S I R R R S N I V P K P E D -

ACCTTGAGAACTAGGGATCTGCCAGAACTAAACAGCATCCTCCCATCTCGATTTTCATTC
2521 -----+-----+-----+-----+-----+-----+-----+ 2580
TGGAACCTCTTGATCCCTAGACGGTCTTGATTGTCTAGGAGGGTAGAGCTAAAAGTAAG

a  T L R T R D L P E L N S I L P S R F S F -
b  P * E L G I C Q N * T A S S H L D F H S -
c  L E N * G S A R T K Q H P P I S I F I P -

CAAAAAGTTGAAACATTAGTCATCACAAATTGCCCCAGAGTTAAGAAACTGCCGTTTCAG
2581 -----+-----+-----+-----+-----+-----+-----+ 2640
GTTTTTCAACTTTGTAATCAGTAGTGTTTAACGGGGTCTCAATTCTTTGACGGCAAAGTC

a  Q K V E T L V I T N C P R V K K L P F Q -
b  K K L K H * S S Q I A P E L R N C R F R -
c  K S * N I S H H K L P Q S * E T A V S G -

GAGAGGAGGACCCAGATGAACTTGCCAACAGTTTATTGTGAGGAGAAATGGTGGAAAGCA
2641 -----+-----+-----+-----+-----+-----+-----+ 2700
CTCTCCTCCTGGGTCTACTTGAACGGTTGTCAAATAACACTCCTCTTTACCACCTTTCGT

a  E R R T Q M N L P T V Y C E E K W W K A -
b  R G G P R * T C Q Q F I V R R N G G K H -
c  E E D P D E L A N S L L * G E M V E S T -

CTGGAAAAAGATCAACCAAACGAAGAGCTTTGTTATTTACGCGCTTTGTTCCAAATTGA
2701 -----+-----+-----+-----+-----+-----+-----+ 2760
GACCTTTTCTAGTTGGTTTGCTTCTCGAAACAATAAATGGCGCGAAACAAGGTTTAACT

a  L E K D Q P N E E L C Y L P R F V P N * -
b  W K K I N Q T K S F V I Y R A L F Q I D -
c  G K R S T K R R A L L F T A L C S K L I -

TATAAGAGCTAAGAGCACTCTGTACAAATATGTCCATTCATAAGATGCAGGAAGCCAGGA
2761 -----+-----+-----+-----+-----+-----+-----+ 2820
ATATTCTCGATTCTCGTGAGACATGTTTATACAGGTAAGTATTCTACGTCTTCGGTCCT

a  Y K S * E H S V Q I C P F I R C R K P G -
b  I R A K S T L Y K Y V H S * D A G S Q E -
c  * E L R A L C T N M S I H K M Q E A R K -

AGGTTGTTCCAGTGAAGTCATCAACTTTCCACATAGCCACAAAAGTAGAGATTATGTAAT
2821 -----+-----+-----+-----+-----+-----+-----+ 2880
TCCAACAAGGTCACCTTCAGTAGTTGAAAGGTGTATCGGTGTTTGTATCTCTAATACATTA

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Fig. 2G

a R L F Q * S H Q L S T * P Q N * R L C N -
b G C S S E V I N F P H S H K T R D Y V I -
c V V P V K S S T F H I A T K L E I M * S -

CATAAAAACCAAACCTATCCGCGA
2881 -----+-----+----- 2903
GTATTTTTGGTTTGATAGGCGCT

a H K N Q T I R -
b I K T K L S A -
c * K P N Y P R -

ENZYMES THAT DO CUT:

NONE

ENZYMES THAT DO NOT CUT:

KpnI

Fig. 2H

-146
 ATCGATTGATCTCTGGCTCAGTGCGAGTAGTCCATTTGAGAGCAGTCGTAGCCCCGCGTG -86

GCGCATCATGGAGCTATTTGGAATTTTCGCAGGGTTATCGATTTCGTAGTGGGAACCCATT -26

CATTGTTTGAACCACCAACGGACGACTTAACAAGCTCCCCGAGGTGCATGATGAAAATT 35
 MetLysIle

GCTCCAGTTGCCATAAATCACAGCCCGCTCAGCAGGGAGGTCCCGTCACACGCGGCACCC 95
 AlaProValAlaIleAsnHisSerProLeuSerArgGluValProSerHisAlaAlaPro

ACTCAGGCAAAGCAAACCAACCTTCAATCTGAAGCTGGCGATTTAGATGCAAGAAAAAGT 155
 ThrGlnAlaLysGlnThrAsnLeuGlnSerGluAlaGlyAspLeuAspAlaArgLysSer

AGCGCTTCAAGCCCGGAAACCCGCGCATTACTCGCTACTAAGACAGTACTCGGGAGACAC 215
 SerAlaSerSerProGluThrArgAlaLeuLeuAlaThrLysThrValLeuGlyArgHis

AAGATAGAGGTTCCGGCCTTTGGAGGGTGGTTCAAAAAGAAATCATCTAAGCACGAGACG 275
 LysIleGluValProAlaPheGlyGlyTrpPheLysLysLysSerSerLysHisGluThr

GGCGGTTCAAGTGCCAACGCAGATAGTTCGAGCGTGGCTTCCGATTCCACCGAAAAACCT 335
 GlyGlySerSerAlaAsnAlaAspSerSerSerValAlaSerAspSerThrGluLysPro

TTGTTCCGTCTCACGCACGTTTCCTTACGTATCCCAAGGTAATGAGCGAATGGGATGTTGG 395
 LeuPheArgLeuThrHisValProTyrValSerGlnGlyAsnGluArgMetGlyCysTrp

TATGCCTGCGCAAGAATGGTTGGCCATTCTGTCTGAAGCTGGGCCTCGCCTAGGGCTGCCG 455
 TyrAlaCysAlaArgMetValGlyHisSerValGluAlaGlyProArgLeuGlyLeuPro

GAGCTCTATGAGGGAAGGGAGGCGCCAGCTGGGCTACAAGATTTTTCAGATGTAGAAAGG 515
 GluLeuTyrGluGlyArgGluAlaProAlaGlyLeuGlnAspPheSerAspValGluArg

TTTATTACAATGAAGGATTAACCTCGGGTAGACCTTCCAGACAATGAGAGATTTACACAC 575
 PheIleHisAsnGluGlyLeuThrArgValAspLeuProAspAsnGluArgPheThrHis


Fig. 3A

GAAGAGTTGGGTGCACTGTTGTATAAGCACGGGCCGATTATATTGGGTGGAAAACCTCCG 635
GluGluLeuGlyAlaLeuLeuTyrLysHisGlyProIleIlePheGlyTrpLysThrPro

AATGACAGCTGGCACATGTCGGTCCTCACTGGTGTGATAAAGAGACGTCGTCCATTACT 695
AsnAspSerTrpHisMetSerValLeuThrGlyValAspLysGluThrSerSerIleThr

TTTCACGATCCCCGACAGGGGCCGGACCTAGCAATGCCGCTCGATTACTTTAATCAGCGA 755
PheHisAspProArgGlnGlyProAspLeuAlaMetProLeuAspTyrPheAsnGlnArg

TTGGCATGGCAGGTTCCACACGCAATGCTCTACCGCTAAGTAGCAGGGTATCTTCACGTG 815
LeuAlaTrpGlnValProHisAlaMetLeuTyrArgEnd

GCGGCATCATGACAAGCCCATGATGCCGCCAGCAGCTACCTGAATGCCGCTGGCTTTTT 875


GGTCCCTATTGTCGTATCCGGAAGATGACGTCAAAGAATCTCGGCAAGAGCTTTCTTGCT 935

CGACTCCTCAGCTTCCGGATCGATCAGGTCGCTTGCCAGAGCGCGCTTGTCATGAGCAT 995

CTGCCACAGCTGCTGGTCGATGGTGTCTCAGCTAAAGGGATTTTGACGACAACCATGCG 1055

CAACTGCCCCGTTGCGATACGCTCGATCCTGAAGCCCCGGTGTCCATGGCAGCCCCAAGAA 1115

AAAGACATAGTTCGCCGCTGTGAGGTTGTAGCCTGTGCCGGCGGCCGACCTGGTCCCGAT 1175

AAACACCCTGCAGTCCGGATCCTGCTGGAAGCATCAATCGCCTTCTGCCGCTTCTTGGG 1235

CGAGTCACTGCCCACCAACGTCACGCACCCGACGCCAAGCTTGAGGCAGTGCTCCCGCAA 1295

CGTGGCCACGGATTCCTGATACTCGCAGAAGAGGATCACCTTGTCGTCGAC 1346

Fig. 3B

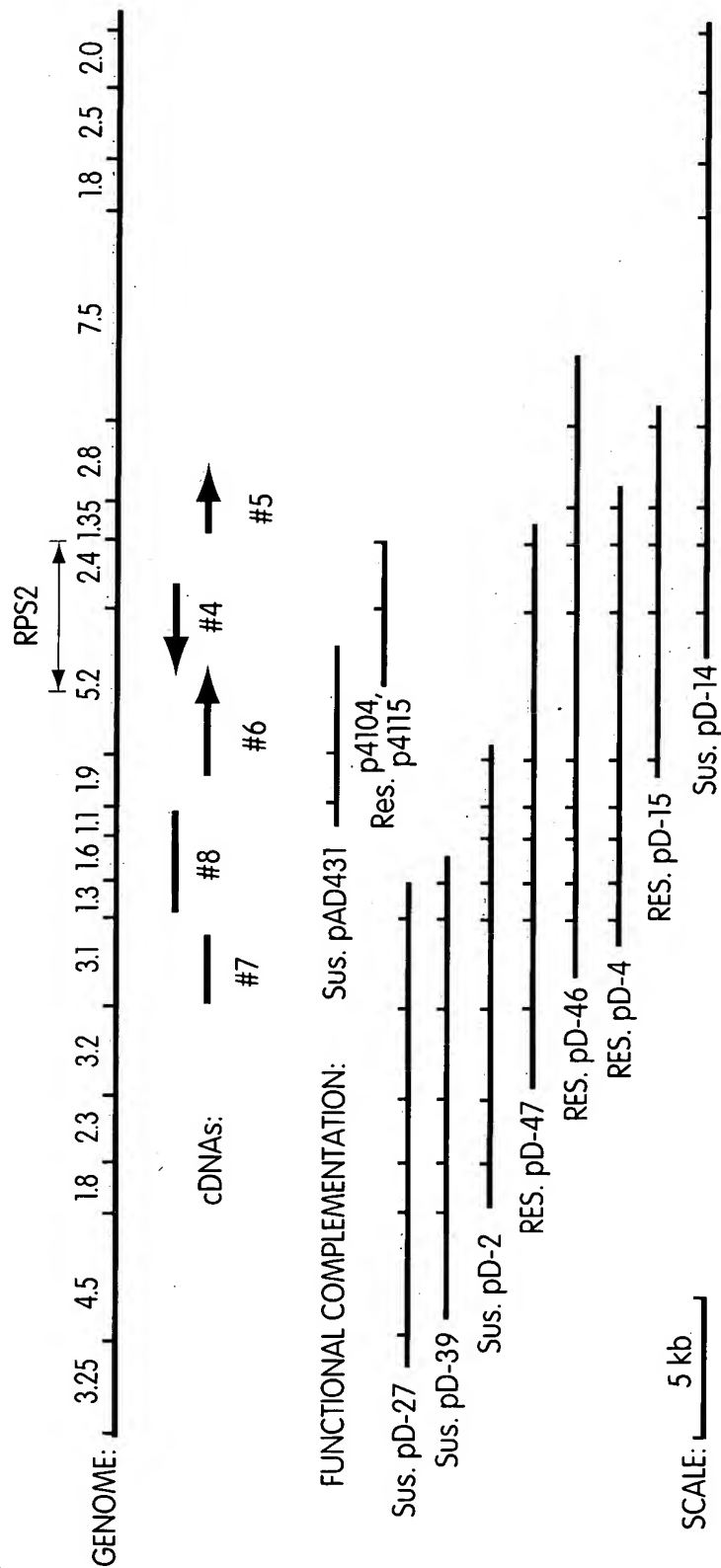


Fig. 4

	1				50
L6pro	MSYLREVATA	VALLLPFILL	NKFWRPNSKD	SIVNDDDDST	SEVDAISDST
NprotM
PrfP
rps2
	51	6			100
L6pro	NPSGSFPSVE	YEVFLSFRGP	DTREQFTDFL	YQSLRRYKIM	TFRDDDELLK
Nprot	ASSSSSSRWS	YDVFLSFRGE	DTRKTFTSHL	YEVLNKGIK	TFQDDKRLEY
PrfP	LRSKLDLIID	LKHQIESVKE
rps2	MDFISSLIVG	CAQVLCESMN	MAERRGHKTD	LRQAITDLET
	101				150
L6pro	GKEIGPNLLR	AIDQSKIYVP	IISSGYADSK	WCLMELAEIV	RRQEEDPRRI
Nprot	GATIPGELCK	AIEESQFAIV	VFSENYATSR	WCLNELVKIM	ECK.TRFKQT
PrfP	GLLCLRSFID	HFSESYDEHDEA	CGLIARVSVM	AYKAE.....
rps2	AIGDLKAIRD	DLTLRIQQDG	LEGRSCSNRA	REWLSAVQVT	ETKTA.....
	151	7			200
L6pro	ILPIFYMVDP	SDVRHQTCGY	KKAFRKHANK	F..DGQTIQN	WKDALKKVG
Nprot	VIPIFYDVDP	SHVRNQKESF	AKAFEEHETK	YKDDVEGIQR	WRIALNEAAN
PrfPYVIDS	CLAYSHPLWY	KVLW.....	..IS.....	..EVLENIKLV
rps2LLLVR	FRRREQRTRM	RRRY.....	..LSCFGCAD	YKLCKKVSAT
	201			8	250
L6pro	LKGWHIGKND	KQGAIADKVS	ADIWSHISKE	NLILE...TD	ELVGIDDHIT
Nprot	LKGSCDNRDK	TDADCIRQIV	DQISSKLCKI	SLSY....LQ	NIVGIDTHLE
PrfP	NKVVGETCER	RNIEVTVHEV	AKTTTYVAPS	FSAYTQRANE	EMEGFQDTID
rps2	LKSIGELRER	SEAIKTDGGS	IQVTCREIPI	KSVVG.....NTTMM
	251		1	-P-loop	300
L6pro	AVLEKLSLDS	ENVTMVGLYG	MGGIGKTTTA	KAVYNKI...	..SSC.FDCC
Nprot	KIESLLEIGI	NGVRIMGIWG	MGGVGKTTIA	RAIFDTLLGR	MDSSYQFDGA
PrfP	ELKDKLLGGS	PELDVISIVG	MPGLGKTTLA	KKIYNDPEVT	..SRFDVHAQ
rps2	EQVLEFLSEE	EERGIIGVYG	PGGVGKTTLM	QSINNELITK	..G....HQY
	301				350
L6pro	CFIDNIRETQ	EKDGVVVLQK	KLVSEILRID	..SGSVGFNN	DSGGRKTIKE
Nprot	CFLKDIKE..	NKRGMHSLQN	ALLSELLR..	...EKANYNN	EEDGKHQMAS
PrfP	CVVTQLYSWR	EL.LLTILND	VLEP...S..	...DRNEKED	GE.IADELRR
rps2	DVLIWVQMSR	EF.GECTIQQ	AVGA...RLG	..LSWDEKET	GENRALKIYR
	351	2		3	400
L6pro	RVSRLFILVV	LDDVDEKFKF	EDMLGSPKDF	ISQ.SRFIIT	SRSMRVLGTL
Nprot	RLRSKKVLIV	LDDIDNKDHY	LEYLAGDLDW	FGNGSRIIIT	TRDKHLI...
PrfP	FLLTRFLIL	IDDVWDYKVV	DNLCMCFSD.	VSNRSRIILT	TRLNDVAEYV
rps2	ALRQKRFLLL	LDDVWEEIDL	EKTGVPRPD.	RENKCKVMFT	TRSIALCENN

Fig. 5A-1

	401					450
L6pro	NEN.QCKLYE	VGSMKPRSL	ELFSKHAFKK	NT....PPSY	YETLANDVVD	
Nprot	.EK.NDIIYE	VTALPDHESI	QLFKQHAFGK	EV....PNEN	FEKLSLEVVN	
PrfP	.KC.ESDPHH	LRLFRDDESW	TLLQKEVFQG	E....SCPPE	LEDVGFEISK	
rps2	.GA.EYK.LR	VEFLEKKHAW	ELFCSKVWRK	DLLESSSIRR	LAEI...IVS	
	451	4				500
L6pro	TTAGLPLTLK	VIGSLLFKQE	IAV..WEDTL	EQL....RRT	LNLDEVYDRL	
Nprot	YAKGLPLALK	VWGSLLHNL	LTE..WKSAL	EHM....KNN	.SYSGIIDNV	
PrfP	SCRGLPLSVV	LVAGVLKQKK	KTLDWKVVE	QSL..SQRI	GSLEESISII	
rps2	KCGGLPLALI	TLGGAMAH.R	ETEEEWIHAS	EVLTRFPAEM	KGMNYVFALL	
	501	5	9			550
L6pro	KISYDALNPE	.AKEIFLDIA	CFFIGQ..NK	EEPYMWTDC	NFYASNIIF	
Nprot	KISYDGLEPK	.QQEMFLDIA	CFLRGE..EK	DYILQILESC	HIGAEGYGLRI	
PrfP	GFSYKNL.PH	YLKPCFLYFG	GFLQKDIHD	SKMTKLWVAE	EFVQANN...	
rps2	KFSYDNLESD	LLRSCFLYCA	LFPEEHSIEI	EQLVEYWVGE	GFLTSSHGVN	
	551		10			600
L6pro	LIQRCMIQVGDD	DEFKMHDQLR	DMGREIVRRE	DVLPWKRSL	
Nprot	LIDKSLVFISEY	NQVQMHDLIQ	DMGKYIVNFQ	KD.PGERSRL	
PrfPEK	GQEDTRTRF.	.LGRSYW...	
rps2	TIYKGYFLIG	DLKAACLLET	GDEKTQVKMH	NVVRSFALWM	ASEQGTYKEL	
	601					650
L6pro	WSAEEGIDLL	LNKKGSSKVK	AISI.PWGVK	YEFK.SECFL	NLSELRYLHA	
Nprot	WLAKEVEEVM	SNNTGTMAE	AIWVSSYSST	LRFS.NQAVK	NMKRLRVFNM	
PrfP	
rps2	ILVEPSMGHT	EAPKAENWRQ	ALVISLLDNR	IQTL.PEKLI	CPKLTTLMLQ	
	651					700
L6pro	REAMLTGDFN	NLLPNLKWLE	LPFYKHGEDD	PPLTNYTMKN	LII.VILEHS	
Nprot	GRSSTHYAID	YLPNNLRCFV	CTNYPW...E	SFPSTFELKM	LVH.LQLRH.	
PrfP	
rps2	QNSSLKKIPT	GFFMHMPVLR	VLDLSF....	TSITEIPLSI	KYL.VELYHL	
	701					750
L6pro	HITADDWGGW	RHMMKMAERL	KVRLASNYS	LYGRRVR...	
NprotNSL	RHLWTETKHL	PSL.....	...RRID...	
PrfP	
rps2	SMSGTKISVL	PQELGNLRKL	KHLDLQRTQF	LQTIPRDAIC	WLSKLEVLNL	
	751					800
L6pro	.LSD.CWRFP	KSIEVLSMTA	IEMDEVDIGE	LKKLKTLLVK	FCPIQKISGG	
Nprot	.LSW.SKRLT	RTPDFTGMPN	LEY..VNLYQ	CSNLEEVHHS	LGCCSKVIGL	
PrfP	
rps2	YYSY.AGWEL	QSFGEDEAEE	LGFADLEYLE	NLTTLGITVL	SLETCLKLFE	

Fig. 5A-2

	801		850
L6pro	TFGMLKGLRE	L.CLEFNWGT	NLREVVADIG QLSSLKVLKT TGAKEVEINE
Nprot	YLNDCKSLKR	F.....PCVNVESLE
PrfP
rps2	FGALHKHIQH	L.HVEECNEL	LYFNLPSLTN HGRNLRRLSI KSCHDLEYLV
	851		900
L6pro	FPLGLK....	...ELSTSSR	IPNLSQLLDL EVLKVYDCKD GFDMPASPSPS
Nprot	Y.LGLR....	...SCDSLEK	LPEIYGRMKP EI..... QIHMQSGSIR
PrfP
rps2	TPADFENDWL	PSLEVLTLS	LHNLTRVWGN SVSQDCLRNI RCINISHCNK
	901		950
L6pro	EDESSVWWKV	SKLKSQLEK	TRINNVVDD ASSGGHLPRY LLPTSLTYLK
Nprot	ELPSSIFQYK	THVTKLL..	.WNMKNLVAL PSSICRL... ..KSLVSLS
PrfP
rps2	LKNVSWVQKL	PKLEVIEFDF	CREIEELISE HESPSVEDPT LFP.SLKTLR
	951		1000
L6pro	IYQCTEPTWL	P.GIENLENL	TSLEVNDIFQ TLGGDLGLQ GLRSLEILRI
Nprot	VSGCSKLESL	PEEIGDLNL	RVFDASDTL.ILRP
PrfP
rps2	TRDLPELNSI	LPSRFSFQKV	ETLVITNCPR VKKLPFQERR TQMNLPVTVC
	1001		1050
L6pro	RKVNGLARIK	GLKDLLCSST	CKLRKFYITE CPDLIELLPC ELGGQTVVVP
Nprot	P.....SSI	IRLNKLIILM FRGFKDGVHF EFPPVAEGLH
PrfP
rps2	EEKWWKALEK	DQPNEELCYL	PRFVPN.... ..
	1051		1100
L6pro	SMAELTIRDC	PRLEVGP MIR	SLPKFPMLKK LDLAVANITK EEDLDAIGSL
Nprot	SLEYLNL.SY	CNLIDGGLPE	EIGSLSSLKK LDLSRNNF.. EHLPPSSIAQL
PrfP
rps2
	1101		1150
L6pro	EELVSLELEL	DDTSSGIERI	VSSSKLQKLT TLVVKVPSLR EIEGLEELKS
Nprot	GALQSLDLK.DCQRLTQLP ELPPELNEH .VDCHMALKF
PrfP
rps2
	1151		1200
L6pro	LQDLYLEGCT	SLGRLPLEKL	KE.....LD IGGCPDLTEL VQTVVAVPSL
Nprot	IHDL.VTKRK	KLHRVKLDDA	HNDTMYNLFA YTMFQNISSM RHDISASDSL
PrfP
rps2

Fig. 5A-3

	1201				1250
L6pro	RGLTIRDCPR	LEVGPMIQSL	PKFPMNLNLT	LSMVNITKED	ELEVLGSLEE
Nprot	.SLTV.....	FTGQPYPEKI	PSWFHHQGWD	.SSVSVNLPE	NWYIPDKFLG
PrfP
rps2
	1251				1300
L6pro	LD.SLELTLD	DTCSSIERIS	FLSKLQKLTT	LIVEVPSLRE	IEGLAELKSL
Nprot	FAVCYSRSLI	DTTAHLIPVC	.DDKMSRMTQ	KLALSECDTE	SSNYSEWD.I
PrfP
rps2
	1301				1350
L6pro	RILYL.....EGCTSLERL	WPDQQQLGSL	KNLNVLDIQG
Nprot	HFFVFPFAGL	WDTSKANGKT	PNDYGIIRLS	FSGEEKMYGL	RLLYKEGPEV
PrfP
rps2
	1351			1387	
L6pro	CKSLSVDHLS	ALKTTLPpra	RITWPDQPYR	
Nprot	NALLQMRENS	NEPTEHSTGI	RRTQYNNRts	FYELING	
PrfP	
rps2	

Fig. 5A-4

Fig. 5B-1

N 539 SSTLRFSNQAVKNMKRLRVFNMGRSSTHYAIDYLPNNLRFCVCTNYPW.. 586
 : .. |...: | : | : : : : : : : : : : : : : : : :
 L6 591 GVKYEFKSECFLNLSELRYLHAREAMLTGDFNNLLPNLKWLELPFYKHGE 640
 N 587 .ESFPSTFELKMLVHLQLRH.....NSLRHLWTETKHLPSL..... 621
 : .. : : : : | : : : | : : : : : : : : : : : : : : : :
 L6 641 DDPPLTNYTMKNLIIVILEHSHITADDWGGWRHMMKMAERLKVVRLASNY 690
 N 622RRIDL\$WSKRLTRTPDFTGMPNLEY..VNLYQCSNLEEVH\$SLGCC 665
 | : : | : | :
 L6 691 SLYGRRVRLSDCWRFPK\$SIEVLSMTA\$EMDEVDIGELKKLKT\$LVLFKFCPI 740
 N 666 SKVIGLYLNDCKSLKRFP\$CVN\$VESLEYLGLRSCDSLEKLPEIYGRMKP.. 713
 | : | :
 L6 741 QKISGGT\$FGMLKGLREL.....CLEFNWGTNLREV\$VADIGQLSSLK 781
 N 714EIQIHMQ\$SGIRELP.SSIFQYKTHVTKLLLWNM....KNLV 750
 | : : : : : : : : : : | : : : : : : : : : : : : : : : :
 L6 782 VLKTTGAKEVEINEFPLGLKELSTSSRIPNLSQLLDLEVLKVYDCKDGF 831
 N 751 ALPSSICRLKSLVSLSVSGC\$SKLES\$PEEIGDL\$DNLRVFDASDTLILRP. 799
 | : | :
 L6 832 MPPASPSEDESSV\$WVKV...\$SKLKS\$LEKTRIN\$VNVVDDASSGGHLPRY 878
 N 800PSSIIRLNKLIILMFRGFKDGVHFEFPPVAE 830
 : : | : : : : : | : : : : : : : : : : : : : : : : :
 L6 879 LLPTSLTYLKIYQCTEPTWLPGIENLENLTSLEVNDIFQTLGGDL\$DGL.Q 927
 N 831 GLHSLEYLNL\$SYCNLID..GGLPEEI.GSLS\$SLKKLDL..SRNNFEHLPS 875
 | : : | : | : : : : : | : : : : : : : : : : : : : : : :
 L6 928 GLRSLEILRIRKVNGLARIKGLKDLLCSSTCKLRKFYITECPDLIELLPC 977
 N 876 SIA....QLGALQSLDLKDCQRLTQLP\$ELPPELNELHVDCHMALKFIHYL 921
 :
 L6 978 ELGGQTVVVP\$SMAELTIRDCPRL.EVGPMIRSLPKFPM.....LKKLDLA 1021
 N 922 VTKRKKLHRVKLDDAHNDTMYNLFAYTMFQNISSMRHDISASDSLSLTVF 971
 | . . | . :
 L6 1022 VANITKEEDLDAIG\$SLEELV..SLELELDDTSSGIERIVSS\$SKLQKLTTL 1069
 N 972 TGQPYPEKIP\$SWFHHQGW\$DSSVSVN.....LPENWYIPDKFLGFAVCY 1014
 : : | : | : : : : : | : : : : : : : : : : : : : : : :
 L6 1070 VV.....KVPSLREIEGLEELKSLQDLYLEGCTSLGRLPLEKLKELD\$IGG 1114

Fig. 5B-2

```

N  1015  SRSLIDTTAHLIPVCDDK.....MSRMTQKLA....LSECDTES 1049
      ...|.:. . . :.:.|. . :      :.:.|.:.|.:.|.:.|. . .
L6 1115  CPDLTELVTQTVVAVPSLRGLTIRDPCPRLEVGPMTIQSLPKFPMLNELTSLM 1164

N  1050  SNYSEWDIHFFFVPPFAGLWDTSKANGKTPNDYGIIRLSFSGEEKMYGLRL 1099
      |...|. . . . . :.:.|. . . :.:.|. . . :.:.|. . . :
L6 1165  VNITKEDELEVLSLEELDSLELTLDDTCSSIERISF.LSKLQKLTTTLIV 1213

N  1100  LYKEGPEVNALLQMRENSNEPTEHSTGIRRTQYNNRTSFYELIN 1143
      . . .|.:.:.|. . . . . :.:.|. . . :.:.|. . . :
L6 1214  EVPSLREIEGLAELKSLRILYLEGCTSLER.LWPDQQQLGSLKN 1256
```

Fig. 5B-3

-32 ACAAGTAAAGAAAGCGAGAAATCATCGAA -1
ATGGAATTCATCTCATCTTATCCTTGGCTGCTCAGGTGTGTGTAATCTATGAATATGGCGGAGAGAGGACATAAGACTGATCTTAGACAAGCCATCACTGATCTTGAACA
M D F I S S L I V G C A Q V L C E S M N M A E R R G H K T D L R Q A I T D L E T 120
relatively hydrophobic
GCCATCGGTGACTGAAGCCCATACGTGATGACCTGACTTTACGGATCCAACAGACGGTCTAGAGGACGAAGCTGCTCAATCGTGCCAGAGAGTGGCTTAGTCCGTGCAAGTAACG
A I G D L K A I R D D L T L R I Q Q D G L E G R S C S N R A R E W L S A V Q V T 240
leucine-zipper
GAGACTAAACAGCCCTACTTTTACTGAGGTTAGCGGTGGGAAACAGAGGACCGGAATCAGGAGGAGATACCTCAGTTGTTTCGGTTGTCCCGACTACAACTGTGCAAGAAGTTTCT
E T K T A L L L V R F R R R E Q R T R M R R R Y L S C F G C A D Y K L C K K V S 360
GCCAATTAAGACAGCATGCTGAGACAACGCTCTGAACCTATCAAAACAGATGGCGGTCAATTCAAGTAACCTGTAGAGAGATACCCATCAAGTCCGTTGTGGAAATACCAAG
A I L K S I G E L R E R S E A I K T D G G S I Q V T C R E I P I K S V V G N T T 480
ATGATGGAACAGGTTTGGAAATTTCTCAGTGAAGAAGAAGAGGAATCAATTGGTGTATGGACCTGTGGGGTGGGAACACACACCTTAATCAGAGCATTAACAACGAGCTGATC
M M E Q V L E F L S E E E R G I I G V Y G P G G V G K T T L M Q S I N N E L I 600
kinase-1a
ACAAAGGACATCAGTATGATGATTGGGTTCAAATGTCCAGAGAAATTCGGCGAGTGTACAATTACAGCAAGCCGTTGGAGCACCGTTGGGTTATCTTGGACGAGAAAGGAGACC
T K G H Q Y D V L I W V Q M S R E F G E C T I Q Q A V G A R L G L S W D E K E T 720
GGCGAAACACAGAGCTTTGAAGATATACAGAGCTTTGAGACAGAAACGTTCTTGTGTTCTAGATGATCTGTGGAGAGAGATAGACTTGGAGAAACTGGAGTTCCTCGACCTGACAGG
G E N R A L K I Y R A L R Q K R F L L L L L D D V W E E I D L E K T G V P R P D R 840
kinase-2

Fig. 6A

Fig. 6B

GGGAATCTTAGAAAACTGAAGCATCTGGACCTACAAGAACCTCAGTTCTTCAGACGATCCACAGAGATGCCATATGTTGGCTGAGCAAGCTCGAGGTTCTGAACTTGTAAGTACAGTTAC 1920
G N L R K L K H L D L Q R T Q F L Q T I P R D A I C W L S K L E V L N L Y Y S Y 640

CCCGTTGGGAAGTGCAGAGCTTTGGAGAGATGAACAGAGAACTCGGATTCGCTGACTTGGAACTACTTGGAAAACTAACACACACTCGGTATCACTGTTCTCTCATTTGGAGACCCCTA 2040
A G W E L Q S F G E D E A E E L G E A D L E Y L E N L T T L G I T V L S L E T L 680

AAAACCTCTTCGAGTTCGGTGGCTTGGCAATAACATATACAGCATCTCCACGTTGAAGAGTGAATGAACCTCTCTACTTCAATCTCCCATCACTCACTAACCATGGCAGAACCTGAGA 2160
K T L F E F G A L H K H I Q H L H V E E C N E L L Y F N L P S L T N H G R N L R 720

AGACTTAGCAATAAAGTTGCCATGACTTGAGTACCTGGTCACACCCGAGATTTTGAATAATGATTGGCTTCGGAGTCTAGAGGTTCTGACGTTACACAGCCTTCACAACTTAACCCAGA 2280
R L S I K S C H D L E Y L V T P A D F E N D W L P S L E V L T L H S L H N L T R 760

GTGTGGGGAATTTCTGTAAGCCCAAGATTGTCTGGGAATATCCGTTGCATAAACATTTCACTGCAACAGCTGAAGATGTCTCATGGGTTTCAGAAACTCCCAAAGTAGAGGTGATT 2400
V W G N S V S Q D C L R N I R C I N I S H C N K L K N V S W V Q K L P K L E V I 800

GAACCTTCGACTGCAGACAGATAGAGGAATTGATAAGCGAACACAGAGTCCATCCGTCCGAAGATCCAAACATTGTTCCCAAGCCTGAAGACCTTGAGAACTAGGGATCTGCCAGAACTA 2520
E L F D C R E I E E L I S E H E S P S V E D P T L F P S L K T L R T R D L P E L 840

AACAGCATCTCCCATCTCGATTTTCATTCCAAAAGTTGAACATTAGTCAACAATTCGCCAGAGTTAAGAACTGCCGTTTCAGGAGAGGAGGCCAGATGAACCTTGCCAACA 2640
N S I L P S R F S F Q K V E T L V I T N C P R V K K L P F Q E R R T Q M N L P T 880

Fig. 6C

· · · · · G T T T A T T G T G A G A A T G G T G A A A G C A C T G G A A A A G A T C A A C C A A C G A A G A G C T T T G T T A T T T A C C G C G C T T T G T T C C A A A T T G A T A T A G A C T A A G A G C A C T C T G T A C A A T A 2760
· · · · · V Y C E E K W K A L E K D Q P N E E L C Y L P R F V P N * 909

· · · · · T G T C C A T T C A T A A G T A G C A G G A A G C T G T T C C A G T A A G T C A T C A A C T T T C C A C T A G C A C A A A C T A G A G A T T A T G T A A T C A T A A A C C A A A C T A T C C G C G A T C A A T A 2880

· · · · · G A T C T C A G C A C T A T G A G G A C G A G A C T C A C C G A G T A T C G T C G A T A T A G A A A C T C C A A G C T C C A G T C C G A T C A G T G A A C G A A C A A G T T T A T C A G A T C T C T G C A A C A A T T C T G G G A A T C 3000

· · · · · G T C A C C T C A G A T T A G A C C T C C A G T A A G A A G T G A G A A G C A T G G A C G A C G A C T G T G A A G A A T T G A G C T A A T G A C T G A A C C G G A T C C G G T G A A A T T G C A G A A C C G G A T C G G A G A A G A A G A A 3120

· · · · · T T T T G C A T T T G C A T C T T T A T T T T T A T T G T T A C G T T T G A G C C C C A A T A A T C A T A G A T A T T G T A G A G A C C A A A T T T C A T G G T G G A T C A A T C A A A T T T T C A A A T T T T C G T A G 3240

· · · · · T G T A A T A A C G G A A A A G G A A T A A A A A G G T C A C T G A G T (A)_n

Fig. 6D

consensus PXXaXX LXXLXXLXaXXXX aXXa

505	PKAENW RQALVISLLD NR IQTL	
527	PEKLIC PK LTTLMLQQNSSLKKI	
550	PTGFFMHMPVLRVLDLSFTS ITEI	
574	PLSIKY LVELYHLSMSGTK ISVL	
597	PQELGN LRKLKHLDLQRTQFLQTI	
621	PRDAICWLSKLEVLNLYYSYAGWEL	QSFGEDEAEELG
658	FADLEY LENLTTLGITVLS LETL	KT
683	LFEFGALHKHIQHLHVEECNELLYF	NL
710	P SLTNHGRNLRRLSIKSDHLEYL	VT
736	PADFENDWLPSLEVLTLHSLHNLTRV	WGN
765	SVSQDC LRNIRCINISHCNKLKNV	SWVQKL
795	PK LEV IELFDCREIEELISEHES	PSVED
823	PT LFPSLKTLRTRDLPELNSI L	
845	PSRFS FQKVETLVITNCPRVKKL	

Fig. 7

Leucine zipper 60
MDFISSLIIV CAQVLCESMN MAERRGHKTD LRQAITDLET AIGDLKAIRD DLTLRQQDGG 120
LEGRSCSNRA REWLSAVQVT ETKTALLVR FRRREQTRM RRRYLSFCGC ADYKLCCKVS 180
AILKSIGELR ERSEAIKTDG GSIQVTCREI PIKSVVGNTT MMEQVLEFLS EEEERGIIGV 240
P loop
YGPGGVGKTT LMQSINNELI TKGHQYDVLI WVQMSREFGE CTIQQAVGAR LGLSWDEKET 300
GENRALKIYR ALRQKRFLLL LDDVWEEIDL EKTGVPRPDR ENCKKVMFTT RSIALCENNMG 360
Membrane-spanning
AEYKLRVEFL EKKHAWELFC SKVWRKDLE SSSIRRLAEI IVSKCGGLPL ALITLGGAMA 420
HRETEEEWIH ASEVLTFRPA EMKGMNYVFA LLKFSYDNLE SDLLRSCFLY CALFPPEHSI 480
EIEQLVEYVW GEGFLTSSHG VNTIYKGYFL IGDLSAACLL ETGDEKTQVK MHNVVRSFAL 540
WMASEQGTYS ELILVEPSMG HTEAPKAENW RQALVISLLD NRIQTLPEKL ICPKLTTLML 600
← Leucine-rich repeats →
QQNSSLKKIP TGFFMHMPVL RVLDLSFTSI TEIPLSIKYL VELYHLSMSG TKISVLPQEL 660
GNLRKLKHL D LQRTQFLQTI PRDAICWLSK LEVLNLYSY AGWELQSFGE DEAEELGFAD 720
LEYLENLTTL GITVLSLETL KTLFEFGALH KHIQHLHVEE CNELLYFNLP SLTNHGRNLR 780
RLSIKSDHL EYLVTPADFE NDWLPSLEVL TLHSLHNLTR VWGNSVSQDC LRNIRCINIS 840
(end Leucine-rich repeats)
HCNKLKNVSW VQKLPKLEVI ELFDCREIEE LISEHESPSV EDPTLFPKSLK TLRTRDLPEL 900
NSILPSRFSF QKVETLVITN CPRVKKLPFQ ERRTQMNLPT VYCEEKWWKA LEKDQPNNEEL 909
CYLPRFVPN

Fig. 8



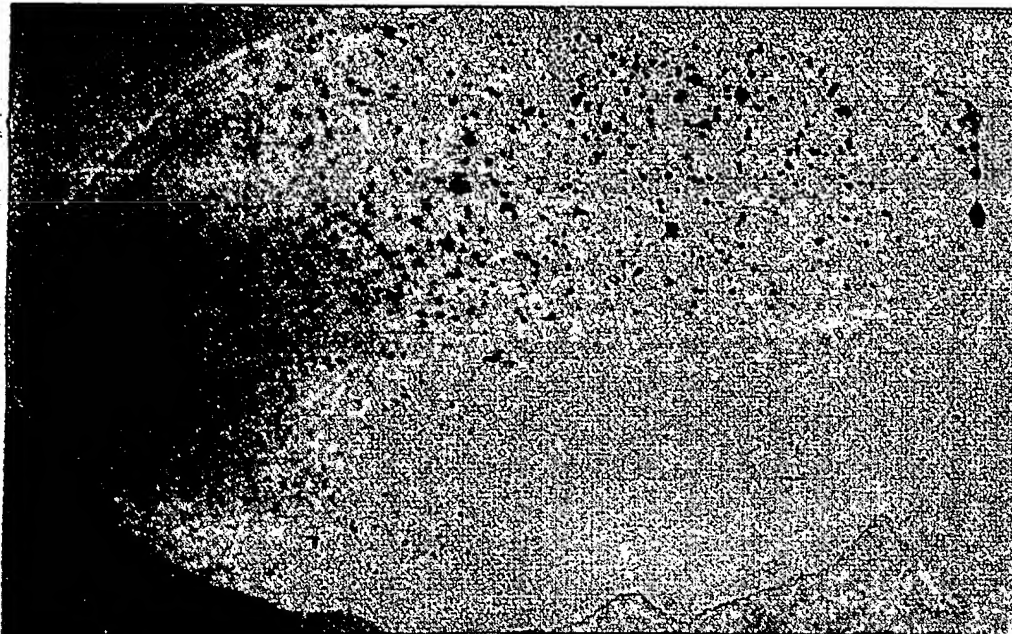


Fig. 10B

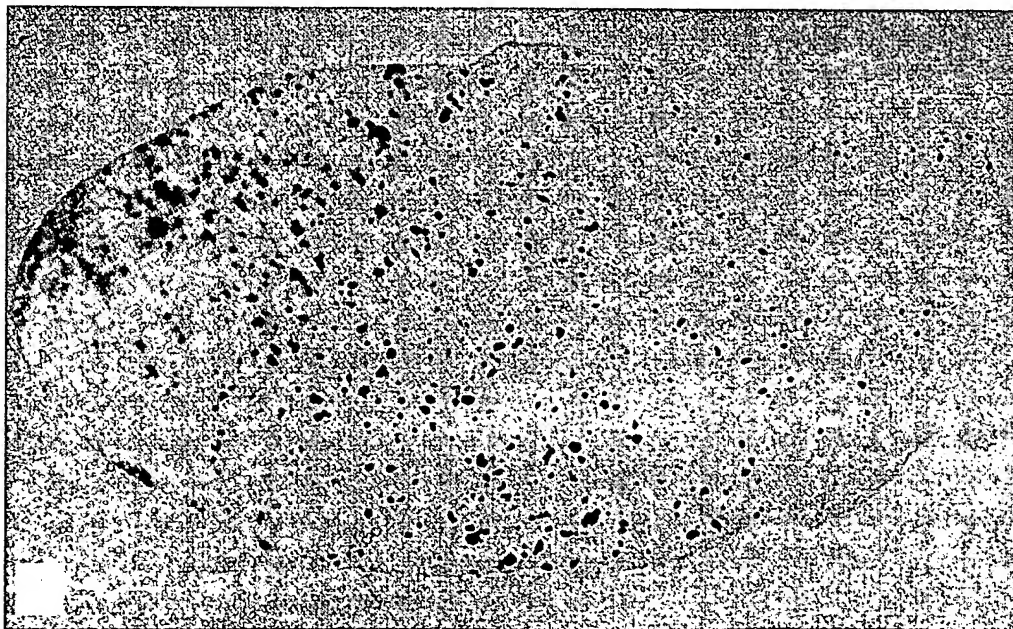


Fig. 10A

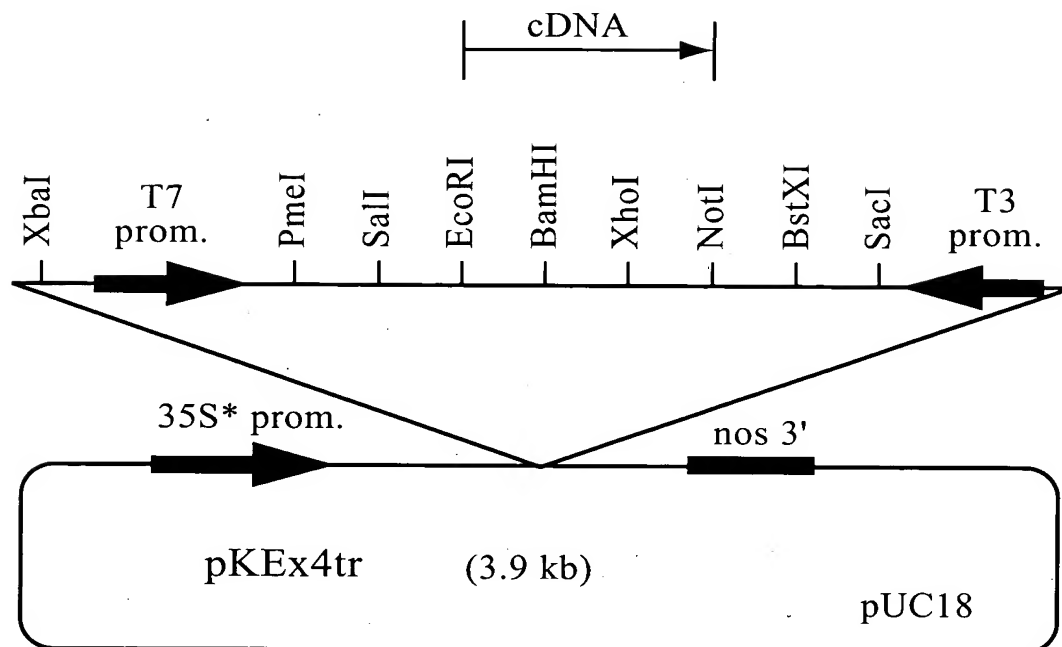


Fig. 11

	10	20	30	40	50	60	
1	aagctttaca	gattggatga	tctcttaatg	catgctgaag	tgactgcaaa	aaggtttagca	60
61	atattcagtg	gttctcgtta	tgaatatctt	atgaacggaa	gcagcactga	gaaaatgagg	120
121	cccttggtat	ctgattttct	gcaagagatt	gagctgtgca	aggtagagtt	cagaaatggt	180
181	tgcttgcaag	ttctggatat	atcacctttt	tccctgacag	atggagaagg	ccttggtaat	240
241	ttcttattaa	aaaaccaggc	caaggtgccg	aatgatgatg	ctgtttcttc	tgatggaagt	300
301	ttagaggatg	caagcagcac	tgagaaaatg	ggacttccat	ctgattttct	ccgagagatt	360
361	gagctctgtg	agataaagga	ggccagaaaa	ttatatgata	aagttttgga	tgcaacacat	420
421	tgtgagacga	gtaagcacga	tggaaaaagc	tttatcaaca	ttatgttaac	ccaacaggac	480
481	aaggtgctgg	actatgatgc	tggttcagtg	tcttatcttc	ttaaccaaat	ctcagtagtt	540
541	aaagacaaaa	tattgcacat	tggctcttta	cttgtagata	ttgtacagta	ccggaatatg	600
601	catatagaac	ttacagatct	cgctgaacgt	gttcaagata	aaaactacat	tcgtttcttc	660
661	tctgtcaagg	gttatattcc	tgttggtat	tacacactat	atctctctga	tgtaagcaa	720
721	ttgcttaagt	ttgttgaggc	agaggtaaag	attatttgct	tgaaagtacc	agattcttca	780
781	agttatagct	tccctaagac	aaatggatta	ggatatctca	attgcttttt	aggcaaattg	840
841	gaggagcttt	tacgttctaa	gctcgatttg	ataatcgact	taaaacatca	gattgaatca	900
901	gtcaaggagg	gcttattgtg	cctaagatca	ttcattgata	atctttcaga	aagctatggt	960
961	gagcatgatg	aagcttggtg	tcttatagca	agagtttctg	taatggcata	caaggctgag	1020
1021	tatgtcattg	actcatgctt	ggcctattct	catccactct	ggtacaaaag	tctttggatt	1080
1081	tctgaagttc	ttgagaatat	taagcttgta	aataaagttg	ttggggagac	atgtgaaaga	1140
1141	aggaacactg	aagttactgt	gcataagatt	gcaaaagact	ccactaatgt	agcaccatct	1200
1201	ttttcagctt	atactcaaag	agcaaacgaa	gaaatggagg	gttttcagga	tacaatagat	1260
1261	gaattaaagg	ataaactact	tggaggatca	cctgagcttg	atgtcatctc	aatcgttggc	1320
1321	atgccaggat	tgggcaagac	tacactagca	aagaagattt	acaatgatcc	agaagtcacc	1380
1381	tctcgtctcg	atgtccatgc	tcaatgtgtt	gtgactcaat	tatattcatg	gagagagttg	1440
1441	ttgctcacca	ttttgaatga	tgtgcttgag	ccttctgata	gcaatgaaaa	agaagatgga	1500
1501	gaaatagctg	atgatctacg	ccgatttttg	ttgaccaaga	gattcttgat	tctcattgat	1560
1561	gatgtgtggg	actataaagt	gtgggacaat	ctatgtatgt	gcttcagtga	tgtttcaaat	1620
1621	aggagtagaa	ttatcctaac	aaccgcgttg	aatgatgtcg	ccgaatatgt	caaatgtgaa	1680
1681	agtgatcccc	atcatcttcg	tttattcaga	gatgacgaga	gttgacattt	attacagaaa	1740
1741	gaagtctttc	aaggagagag	ctgtccacct	gaacttgaag	atgtgggatt	tgaaatatca	1800
1801	aaaagttgta	gagggttgcc	tctctcagtt	gtgttagtag	ctggtgttct	gaaacagaaa	1860
1861	aagaagacac	tagattcatg	gaaagtagta	gaacaaagtc	taagttccca	gaggattggc	1920
1921	agcttggaag	agagcatatc	tataattgga	ttcagttaca	agaatttacc	acactatctt	1980
1981	aagccttggt	ttctctatct	tggaggattt	ttgcagggaa	aggatattca	tgactcaaaa	2040
2041	atgaccaagt	tgtgggtagc	tgaagagttt	gtacaagcaa	acaacgaaaa	aggacaagaa	2100
2101	gatacccgca	caaggtttct	tggacgatct	tatttggtagg	aatctggtga	tggccatgga	2160
2161	gaagagacct	aatgccaaag	tgaaaacgtg	ccgcattcat	gatttggtgc	ataaattctg	2220
2221	catggaaaag	gccaaacaag	aggatttcct	tctccagatc	aataggtaaa	aaaaactgta	2280
2281	ttaattttac	attacaaaaa	aaaagaactg	tattaatttt	actgtattat	gtttatgcca	2340
2341	actctcattt	ccatgtgttc	tcttttatct	aattcagttg	agaaggtgta	tttctgaac	2400
2401	gattggaaga	ataccgattg	ttcgttcatt	cttaccaaga	tgaaattgat	ctgtggcgcc	2460
2461	catctcgtc	taatgtccgc	tctttactat	tcaatgcaat	tgatccagat	aacttggtat	2520
2521	ggccgcgtga	tatctccttc	atcttttgaga	gcttcaagct	tgtaaagtgt	ttggatttgg	2580

Fig. 12A

2581	aatcattcaa	cattggtggt	acttttccca	ttgaaacaca	atatctaatt	cagatgaagt	2640
2641	actttgcggc	ccaaactgat	gcaaattcaa	ttccttcac	tatagctaag	cttgaaaatc	2700
2701	ttgagacttt	tgtecgtaaga	ggattgggag	gagagatgat	attaccttgt	tcacttctga	2760
2761	agatggtgaa	attgaggcat	atacatgtaa	atgatcgggt	ttcttttggt	ttgcgtgaga	2820
2821	acatggatgt	tttaactggt	aactcacaat	aacctaattt	ggaaaccttt	tctactccgc	2880
2881	gtctctttta	tggtaaagac	gcagagaaga	ttttgaggaa	gatgccaaaa	ttgagaaaat	2940
2941	tgagttgcat	attttcaggg	acatttggtt	attcaaggaa	attgaagggt	aggtgtgttc	3000
3001	gttttcccag	attagatttt	ctaagtcacc	ttgagtcctt	caagctgggt	tcgaacagct	3060
3061	atccagccaa	acttcctcac	aagttcaatt	tcccctcgca	actaagggaa	ctgactttat	3120
3121	caaagtccg	tctaccttg	acccaaattt	cgatcattgc	agaactgccc	aacttggtga	3180
3181	ttcttaagtt	attgctcaga	gcctttgaag	gggatcactg	ggaagtgaag	gattcagagt	3240
3241	tcctagaact	caaatactta	aaactggaca	acctcaaagt	tgtacaatgg	tccatctctg	3300
3301	atgatgcttt	tcctaagctt	gaacatttg	ttttaacgaa	atgtaagcat	cttgagaaaa	3360
3361	tcccttctcg	ttttgaagat	gctgtttgtc	taaatagagt	tgaggtgaac	tggtgcaact	3420
3421	ggaatgttgc	caattcagcc	caagatattc	aaactatgca	acatgaagtt	atagcaaatg	3480
3481	attcattcac	agttactata	cagcctccag	attggtctaa	agaacagccc	cttgactctt	3540
3541	agcaaagggt	tgttcttgct	gtgttcaccc	aagtgcattt	aacattttatt	cattttgttt	3600
3601	tacaccagaa	catgtttatt	ttgctagtat	tacttgatac	attaaaagaa	atcgaactca	3660
3661	tattttctgct	acagtcttaa	cttttcttg	gcttacttga	ggtctagatt	agatcaatgg	3720
3721	ttcatgtaat	ttttaattca	ctgtttcatt	caactgtctt	atgatagtgtg	tgaaatgaca	3780
3781	atattgttat	ccctagccaa	atttattatg	ttcaaataag	aactgatgtc	acaactactt	3840
3841	ttttgtgaaa	tgtttttgaa	ttttttgcta	taaaattgac	gaattgacag	cttctatat	3900
3901	tgtcagctaa	actctttgtc	accagaagtg	tatttagaat	tactgtgggt	ttatgaaaga	3960
3961	gttctgtaga	attttatgct	tttgagaat	atagtttaaa	acaacaacac	ttctctgttt	4020
4021	cagagatagc	agaagctaaa	gttcaaggca	ttttgtttat	ttctagaaca	agtggagtgc	4080
4081	ttatgttgaa	ttcttgaaaa	gaagaagaat	caggagcagg	taaagtattc	tctttttatg	4140
4141	tttttcttct	tttagatggt	atttcttcat	cttgaacgtg	aacaccgctg	aaagcatttt	4200
4201	aataaaaccg	gagagaaaaa	taagatcttt	ttatataaag	cattatcatg	taaatatgcc	4260
4261	taaatccata	tggtacaact	gtttgacaaa	atgatagaga	ggggagtgtt	atagtataag	4320
4321	taaaacagga	ttgagaaaaa	aatccttgca	cgattttcaa	tttctggcca	catcacaatg	4380
4381	tggtgtcaaag	ttccctctct	taagtgaac	aagcaatcag	aaaagctcat	tcttatcggt	4440
4441	gacataccaa	taccagctga	ctgtctcatc	ttggttaact	tagccttgct	tacttagact	4500
4501	attagattag	ttactaatga	actggtaaat	tggaacccaa	tgtagttagc	ttgatgagct	4560
4561	ggtagacatg	tatatatgaa	gatacacgag	taacttttagt	cgatgggttaa	tttttcattt	4620
4621	ttgatttttt	ttcttcacag	agtatatatg	aacttggcct	aaaagttttg	cttcactaat	4680
4681	ttactatta	ccgtggatga	aacaagcatg	gcaacatttt	caacaactat	cactcaagca	4740
4741	atgtaaaaaa	tgaggttct	acgagcggta	catgtaagag	ttttgtgcac	acaagaggtt	4800
4801	ctgagacttg	aaccatccat	gtccaaggca	gttgagatgc	tagtaaagaa	agaagaagat	4860
4861	gagcctgcac	taattaatct	ccctgtatga	atgagagaat	gagaaaaaga	tgagagcttc	4920
4921	tgaacccaaa	gttacctttt	ttttttcttc	ttaatggcat	tactttgaag	cacatgtttg	4980
4981	ttagttgtaa	attgtaatgg	tgaagtgttt	gtaaatatag	ggagtgtat	ttgaaagaat	5040
5041	ggttgtgtta	tctttacaaa	ccggaatcat	ttctgtataa	ttttcttctg	taattttttg	5100
5101	tttcggttta	ttcattactc	atttcagtaa	gctt			5134
	10	20	30	40	50	60	

Fig. 12B